```
                    GenCore version 4.5
              Copyright (c) 1993 - 2000  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:         January 29, 2002, 20:56:02 ; Search time 81.07 Seconds
                                             (without alignments)
                                             108.951 Million cell updates/sec

Title:          US-09-432-546-15
Perfect score:  39
Sequence:       1 aggagatggccttggtggccttggaaatggcctcttatt 39

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters:      702406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_NA:*
                 1:  /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                 2:  /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                 3:  /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                 4:  /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                 5:  /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 6:  /cgn2_6/ptodata/2/ina/backfiles1.seq:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                                SUMMARIES
                 %
Result         Query
  No.   Score  Match Length DB ID                           Description
-------------------------------------------------------------------------------
c   1    20.8   53.3   1680  4 US-09-603-185-1               Sequence 1, Appli
    2    20.6   52.8  15328  2 US-08-888-497-33              Sequence 33, Appl
    3    20.6   52.8  15328  5 PCT-US94-07926-33             Sequence 33, Appl
    4    19.8   50.8    107  4 US-08-943-731-47              Sequence 47, Appl
    5    19.8   50.8   2974  1 US-08-290-978A-4              Sequence 4, Appli
    6    19.8   50.8   2974  2 US-08-780-869-4               Sequence 4, Appli
    7    19.8   50.8  18609  4 US-08-943-731-1               Sequence 1, Appli
    8    19.8   50.8  33529  4 US-09-144-085-3               Sequence 3, Appli
    9    19.6   50.3  71989  4 US-09-443-501A-2              Sequence 2, Appli
   10    19.4   49.7    423  1 US-08-470-179-111             Sequence 111, App
   11    19.4   49.7    423  1 US-08-470-179-147             Sequence 147, App
   12    19.4   49.7    918  4 US-09-248-588-12              Sequence 12, Appl
   13    19.4   49.7   1263  5 PCT-US96-10602-9              Sequence 9, Appl
   14    19.4   49.7   1801  1 US-08-391-000-41              Sequence 41, Appl
   15    19.4   49.7   1801  2 US-08-741-931-41              Sequence 41, Appl
c  16    19.2   49.2   3113  1 US-08-146-422-20              Sequence 20, Appl
c  17    19.2   49.2   3113  1 US-08-626-554-2               Sequence 2, Appli
   18    19.2   49.2 246240  2 US-08-724-394A-20             Sequence 20, Appl
   19    19.2   49.2 246240  2 US-08-724-394A-21             Sequence 21, Appl
   20    19.2   49.2 246240  2 US-08-724-394A-22             Sequence 22, Appl
   21      19   48.7    702  2 US-09-024-848-3               Sequence 3, Appli
   22      19   48.7    702  4 US-09-348-116A-3              Sequence 3, Appli
   23      19   48.7    879  2 US-09-024-848-1               Sequence 1, Appli
   24      19   48.7    879  4 US-09-348-116A-1              Sequence 1, Appli
c  25      19   48.7   1102  2 US-08-742-440A-5              Sequence 5, Appli
c  26      19   48.7   1131  1 US-08-181-271A-22             Sequence 22, Appl
c  27      19   48.7   1131  1 US-08-449-315-22              Sequence 22, Appl
c  28      19   48.7   1131  1 US-08-444-803-22              Sequence 22, Appl
c  29      19   48.7   1131  1 US-08-449-043-22              Sequence 22, Appl
c  30      19   48.7   1131  1 US-08-456-265A-22             Sequence 22, Appl
c  31      19   48.7   1131  1 US-08-455-416-22              Sequence 22, Appl
c  32      19   48.7   1131  1 US-08-455-244-22              Sequence 22, Appl
c  33      19   48.7   1131  1 US-08-454-876-22              Sequence 22, Appl
c  34      19   48.7   1131  2 US-08-457-364-22              Sequence 22, Appl
c  35      19   48.7   1131  2 US-08-456-262-22              Sequence 22, Appl
c  36      19   48.7   1131  2 US-08-456-240-22              Sequence 22, Appl
c  37      19   48.7   1131  2 US-08-455-736-22              Sequence 22, Appl
c  38      19   48.7   1131  2 US-08-971-217-22              Sequence 22, Appl
c  39      19   48.7   1131  4 US-09-350-600-22              Sequence 22, Appl
c  40      19   48.7   1224  2 US-08-742-440A-4              Sequence 4, Appli
   41      19   48.7   1437  4 US-09-446-504-63              Sequence 63, Appl
c  42      19   48.7   1839  1 US-08-152-019A-44             Sequence 44, Appl
c  43      19   48.7   1839  3 US-08-482-677-1               Sequence 1, Appli
   44      19   48.7   3574  4 US-09-446-504-83              Sequence 83, Appl
   45      19   48.7   8460  1 US-08-469-005A-9              Sequence 9, Appli

                                ALIGNMENTS

RESULT 1
US-09-603-185-1/c
; Sequence 1, Application US/09603185
; Patent No. 6271004
; GENERAL INFORMATION:
;  APPLICANT: Warthoe, Peter
;  TITLE OF INVENTION: A METHOD FOR IMPROVED REVERSE TRANSCRIPTION AT HIGH TEMPERATUR
;  FILE REFERENCE: 674513-2002
;  CURRENT APPLICATION NUMBER: US/09/603,185
;  CURRENT FILING DATE:  2000-06-26
;  PRIOR APPLICATION NUMBER: DK199900897
;  PRIOR FILING DATE: 1999-06-25
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 1680
;   TYPE: DNA
;   ORGANISM: Pyrococcus sp.
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (39)..(1637)
US-09-603-185-1


  Query Match             53.3%;  Score 20.8;  DB 4;  Length 1680;
  Best Local Similarity   78.1%;  Pred. No. 24;
  Matches   25;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          3 gagatggccttggtggccttggaaatggcctc 34
              | |||| |||||  ||||| || || ||||||
Db       1381 GGGATGACCTTGAGGGCCTCGGCAAAGGCCTC 1350


RESULT 2
US-08-888-497-33
; Sequence 33, Application US/08888497
; Patent No. 5972677
; GENERAL INFORMATION:
;   APPLICANT:  Tischfield, Jay A.
;   APPLICANT:  Seilhamer, Jeffrey J.
;   TITLE OF INVENTION:  Mammalian Phospholipase A2 Nucleotide
;   TITLE OF INVENTION:  Sequences and Low Molecular Weight Amino Acid Sequences
;   TITLE OF INVENTION:  Encoded Thereby, Antisense Sequences and Nucleotide
;   TITLE OF INVENTION:  Sequences Having Internal Ribosome Binding Sites
;   NUMBER OF SEQUENCES:  44
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Ruden, Barnett, McClosky, Smith, Schuster &
;     ADDRESSEE:  Russell PA
;     STREET:  200 East Broward Boulevard
;     CITY:  Fort Lauderdale
```

```
;       STATE:  FL
;       COUNTRY:  USA
;       ZIP:  33301
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/888,497
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/651,405
;       FILING DATE:
;       APPLICATION NUMBER:  US 08/097,354
;       FILING DATE:  26-JUL-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Manso, Peter J.
;       REGISTRATION NUMBER:  32,264
;       REFERENCE/DOCKET NUMBER:  IN21044-5
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  305-527-2498
;       TELEFAX:  305-764-4996
;   INFORMATION FOR SEQ ID NO:  33:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  15328 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-888-497-33

  Query Match             52.8%;  Score 20.6;  DB 2;  Length 15328;
  Best Local Similarity   85.2%;  Pred. No. 43;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 gagatggccttggtggccttggaaatg 29
              ||| ||| ||||| |||| ||||||||
Db      15060 GAGCTGGACTTGGAGGCCATGGAAATG 15086


RESULT   3
PCT-US94-07926-33
; Sequence 33, Application PC/TUS9407926
;  GENERAL INFORMATION:
;    APPLICANT:  Tischfield, Jay A.
;    APPLICANT:  Seilhamer, Jeffrey J.
;    TITLE OF INVENTION:  Mammalian Phospholipase A2 Nucleotide
;    TITLE OF INVENTION:  Sequences and Low Molecular Weight Amino Acid Sequences
;    TITLE OF INVENTION:  Encoded Thereby, Antisense Sequences and Nucleotide
;    TITLE OF INVENTION:  Sequences Having Internal Ribosome Binding Sites
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ruden, Barnett, McClosky, Smith, Schuster &
;      ADDRESSEE:  Russell PA
;      STREET:  200 East Broward Boulevard
;      CITY:  Fort Lauderdale
;      STATE:  FL
;      COUNTRY:  USA
;      ZIP:  33301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/07926
;      FILING DATE:  15-JUL-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/097,354
```

```
;       FILING DATE:  26-JUL-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Manso, Peter J.
;       REGISTRATION NUMBER:  32,264
;       REFERENCE/DOCKET NUMBER:  IN21044-5
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  305-527-2498
;       TELEFAX:  305-764-4996
;   INFORMATION FOR SEQ ID NO:  33:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  15328 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
PCT-US94-07926-33

  Query Match             52.8%;  Score 20.6;  DB 5;  Length 15328;
  Best Local Similarity   85.2%;  Pred. No. 43;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 gagatggccttggtggccttggaaatg 29
              ||| ||| ||||| |||| ||||||||
Db      15060 GAGCTGGACTTGGAGGCCATGGAAATG 15086


RESULT   4
US-08-943-731-47
; Sequence 47, Application US/08943731
; Patent No. 6265157
;  GENERAL INFORMATION:
;    APPLICANT:  PROCKOP, DARWIN J.
;    APPLICANT:  SPOTILA, LORETTA D.
;    APPLICANT:  DELTAS, CONSTANTINOS D.
;    APPLICANT:  SEREDA, LARISA
;    APPLICANT:  LARSON, ANDREA W.
;    APPLICANT:  PACK, MICHAEL
;    APPLICANT:  COLIGE, ALAIN
;    APPLICANT:  EARLY, JAMES
;    APPLICANT:  KORKKO, JARMO
;    APPLICANT:  ALA-KOKKO, LEENA, et al.
;    TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR DETECTING
;    TITLE OF INVENTION:  ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
;    NUMBER OF SEQUENCES:  666
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PANITCH SCHWARZE JACOBS & NADEL, P.C.
;      STREET:  ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
;      STREET:  FLR.
;      CITY:  PHILADELPHIA
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103-7086
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,731
;      FILING DATE:  03-OCT-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/212,322
;      FILING DATE:  14-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/803,628
;      FILING DATE:  03-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DOYLE LEARY Ph.D., KATHRYN
;      REGISTRATION NUMBER:  36,317
;      REFERENCE/DOCKET NUMBER:  9598-27
;    TELECOMMUNICATION INFORMATION:
```

```
;      TELEPHONE:  215-965-1284
;      TELEFAX:  215-567-2991
;      TELEX:  831-494
;  INFORMATION FOR SEQ ID NO:  47:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-943-731-47

  Query Match              50.8%;  Score 19.8;  DB 4;  Length 107;
  Best Local Similarity    77.4%;  Pred. No. 35;
  Matches   24;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       6 atggccttggtggccttggaaatggcctctt 36
           |||||| | |||||||||   | | ||||||
Db      38 ATGGCCATTGTGGCCTTGCCTAAGCCCTCTT 68


RESULT   5
US-08-290-978A-4
; Sequence 4, Application US/08290978A
; Patent No. 5624834
;  GENERAL INFORMATION:
;    APPLICANT:  KUSTERS-VAN SOMEREN, MARGO A.
;    APPLICANT:  MULLER, YVONNE
;    APPLICANT:  KESTER, HERMANUS C.M.
;    APPLICANT:  VISSER, JACOB
;    APPLICANT:  VAN OOYEN, ALBERT J.J.
;    APPLICANT:  ROLIN, CLAUS
;    TITLE OF INVENTION:  CLONING AND EXPRESSION OF THE
;    TITLE OF INVENTION:  EXO-POLYGALACTURONASE GENE FROM ASPERGILLUS
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Avenue N.W
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1812
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/290,978A
;      FILING DATE:  17-OCT-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  4615-0044.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;      TELEX:  90-4030
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2974 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  ORGANISM:  Aspergillus tubigensis
;      STRAIN:  NW756
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  640..945
;    FEATURE:
;      NAME/KEY:  intron
;      LOCATION:  946..1002
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  1003..1371
;    FEATURE:
;      NAME/KEY:  intron
;      LOCATION:  1372..1423
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  1424..1480
;    FEATURE:
;      NAME/KEY:  intron
;      LOCATION:  1481..1538
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  1539..1940
;    FEATURE:
;      NAME/KEY:  intron
;      LOCATION:  1941..1990
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  1991..2092
;    FEATURE:
;      NAME/KEY:  intron
;      LOCATION:  2093..2144
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  2145..2219
;    FEATURE:
;      NAME/KEY:  intron
;      LOCATION:  2220..2272
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  2273..2317
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(640..945, 1003..1371, 1424..1480, 1539..1940,
;      LOCATION:  1991..2092, 2145..2219, 2273..2317)
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  640
;      OTHER INFORMATION:  /note= "codon start= 640; product=
;      OTHER INFORMATION:  "exo-polygalacturonase precursor"; gene= "pgaX""
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  640..705
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  706..2317
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  706..2317
;      OTHER INFORMATION:  /note= "IDENTIFICATION METHOD:
;      OTHER INFORMATION:  experimental; product= "exo-polygalacturonase mature enzym
;      OTHER INFORMATION:  evidence= EXPERIMENTAL"
US-08-290-978A-4

  Query Match              50.8%;  Score 19.8;  DB 1;  Length 2974;
  Best Local Similarity    69.2%;  Pred. No. 64;
  Matches   27;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy       1 aggagatggccttggtggccttggaaatggcctcttatt 39
           ||  |||  || ||  ||||||  ||||||| || || |
Db       7 AGAGGATCCCCCTGTCGGCCTTTTAAATGGCTTCCTAGT 45


RESULT   6
US-08-780-869-4
```

```
; Sequence 4, Application US/08780869
; Patent No. 5830737
;  GENERAL INFORMATION:
;    APPLICANT:  KUSTERS-VAN SOMEREN, MARGO A.
;    APPLICANT:  MULLER, YVONNE
;    APPLICANT:  KESTER, HERMANUS C.M.
;    APPLICANT:  VISSER, JACOB
;    APPLICANT:  VAN OOYEN, ALBERT J.J.
;    APPLICANT:  ROLIN, CLAUS
;    TITLE OF INVENTION:  CLONING AND EXPRESSION OF THE
;    TITLE OF INVENTION:  EXO-POLYGALACTURONASE GENE FROM ASPERGILLUS
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Avenue N.W.
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1812
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/780,869
;      FILING DATE:  24-JAN-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/290,978
;      FILING DATE:  17-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  4615-0044.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;      TELEX:  90-4030
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2974 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  ORGANISM:  Aspergillus tubigensis
;      STRAIN:  NW756
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  640..945
;    FEATURE:
;      NAME/KEY:  intron
;      LOCATION:  946..1002
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  1003..1371
;    FEATURE:
;      NAME/KEY:  intron
;      LOCATION:  1372..1423
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  1424..1480
;    FEATURE:
;      NAME/KEY:  intron
;      LOCATION:  1481..1538
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  1539..1940
;    FEATURE:
;      NAME/KEY:  intron
;      LOCATION:  1941..1990
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  1991..2092
;    FEATURE:
;      NAME/KEY:  intron
;      LOCATION:  2093..2144
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  2145..2219
;    FEATURE:
;      NAME/KEY:  intron
;      LOCATION:  2220..2272
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  2273..2317
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(640..945, 1003..1371, 1424..1480, 1539..1940,
;      LOCATION:  1991..2092, 2145..2219, 2273..2317)
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  640
;      OTHER INFORMATION:  /note= "codon start= 640; product=
;      OTHER INFORMATION:  "exo-polygalacturonase precursor"; gene= "pgaX""
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  640..705
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  706..2317
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  706..2317
;      OTHER INFORMATION:  /note= "IDENTIFICATION METHOD:
;      OTHER INFORMATION:  experimental; product= "exo-polygalacturonase mature enzym
;      OTHER INFORMATION:  evidence= EXPERIMENTAL"
US-08-780-869-4


  Query Match            50.8%;  Score 19.8;  DB 2;  Length 2974;
  Best Local Similarity  69.2%;  Pred. No. 64;
  Matches   27;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy       1 aggagatggccttggtggccttggaaatggcctcttatt 39
           ||  |||  || ||  ||||||  ||||||| || || |
Db       7 AGAGGATCCCCCTGTCGGCCTTTTAAATGGCTTCCTAGT 45


RESULT   7
US-08-943-731-1
; Sequence 1, Application US/08943731
; Patent No. 6265157
;  GENERAL INFORMATION:
;    APPLICANT:  PROCKOP, DARWIN J.
;    APPLICANT:  SPOTILA, LORETTA D.
;    APPLICANT:  DELTAS, CONSTANTINOS D.
;    APPLICANT:  SEREDA, LARISA
;    APPLICANT:  LARSON, ANDREA W.
;    APPLICANT:  PACK, MICHAEL
;    APPLICANT:  COLIGE, ALAIN
;    APPLICANT:  EARLY, JAMES
;    APPLICANT:  KORKKO, JARMO
;    APPLICANT:  ALA-KOKKO, LEENA, et al.
;    TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR DETECTING
;    TITLE OF INVENTION:  ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
;    NUMBER OF SEQUENCES:  666
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PANITCH SCHWARZE JACOBS & NADEL, P.C.
;      STREET:  ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
;      STREET:  FLR.
;      CITY:  PHILADELPHIA
```

```
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103-7086
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,731
;      FILING DATE:  03-OCT-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/212,322
;      FILING DATE:  14-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/803,628
;      FILING DATE:  03-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DOYLE LEARY Ph.D., KATHRYN
;      REGISTRATION NUMBER:  36,317
;      REFERENCE/DOCKET NUMBER:  9598-27
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-965-1284
;      TELEFAX:  215-567-2991
;      TELEX:  831-494
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18609 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-943-731-1


  Query Match             50.8%;  Score 19.8;  DB 4;  Length 18609;
  Best Local Similarity   77.4%;  Pred. No. 89;
  Matches   24;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      6 atggccttggtggccttggaaatggcctctt 36
          |||||| | |||||||||   | | ||||||
Db  13042 ATGGCCATTGTGGCCTTGCCTAAGCCCTCTT 13072


RESULT   8
US-09-144-085-3
; Sequence 3, Application US/09144085
; Patent No. 6280999
; GENERAL INFORMATION:
;  APPLICANT: Gustafsson, Claes
;  APPLICANT: Betlach, Mary C.
;  APPLICANT: Ashley, Gary
;  APPLICANT: Julien, Bryan
;  APPLICANT: Ziermann, Rainer
;  TITLE OF INVENTION: SORANGIUM POLYKETIDE SYNTHASES AND ENCODING DNA
;  TITLE OF INVENTION: THEREFOR
;  FILE REFERENCE: 30062-20020.20
;  CURRENT APPLICATION NUMBER: US/09/144,085
;  CURRENT FILING DATE: 1998-08-31
;  EARLIER APPLICATION NUMBER: 09/010,809
;  EARLIER FILING DATE: 1998-01-22
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 33529
;   TYPE: DNA
;   ORGANISM: Sorangium cellulosum
US-09-144-085-3


  Query Match             50.8%;  Score 19.8;  DB 4;  Length 33529;
  Best Local Similarity   69.2%;  Pred. No. 99;
```

```
  Matches   27;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy      1 aggagatggccttggtggccttggaaatggcctcttatt 39
          || || ||||||||   |||||| |||||   ||  | |
Db  15202 agcagctggccttgcaagccttgcaaatgatttcgaact 15240


RESULT   9
US-09-443-501A-2
; Sequence 2, Application US/09443501A
; Patent No. 6303342
; GENERAL INFORMATION:
;  APPLICANT: Kosan Biosciences, Inc.
;  APPLICANT:  Julien, Bryan
;  APPLICANT:  Katz, Leonard
;  APPLICANT:  Khosla, Chaitan
;  APPLICANT:  Tang, Li
;  APPLICANT:  Ziermann, Rainer
;  TITLE OF INVENTION: Recombinant Methods and Materials for Producing
;  TITLE OF INVENTION:  Epothilone and Epothilone Derivatives
;  FILE REFERENCE: 30062-20031.00
;  CURRENT APPLICATION NUMBER: US/09/443,501A
;  CURRENT FILING DATE:  1999-11-19
;  PRIOR APPLICATION NUMBER: US 60/130,560
;  PRIOR FILING DATE: 1999-04-22
;  PRIOR APPLICATION NUMBER: US 60/122,620
;  PRIOR FILING DATE: 1999-03-03
;  PRIOR APPLICATION NUMBER: US 60/119,386
;  PRIOR FILING DATE: 1999-02-10
;  PRIOR APPLICATION NUMBER: US 60/109,401
;  PRIOR FILING DATE: 1998-11-20
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 71989
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-09-443-501A-2


  Query Match             50.3%;  Score 19.6;  DB 4;  Length 71989;
  Best Local Similarity   73.5%;  Pred. No. 1.3e+02;
  Matches   25;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy      1 aggagatggccttggtggccttggaaatggcctc 34
          ||| || | | | |||| || ||||| ||| |||
Db  13997 aggcgacgccgtgggtgcccgtggaagtgggctc 14030


RESULT  10
US-08-470-179-111
; Sequence 111, Application US/08470179
; Patent No. 5645994
;  GENERAL INFORMATION:
;    APPLICANT:  Huang Ph.D, Wai Mun
;    TITLE OF INVENTION:  Method and Compositions for
;    TITLE OF INVENTION:  Identification of Species in a Sample
;    NUMBER OF SEQUENCES:  207
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Trask, Britt and Rossa
;      STREET:  P.O. Box 2550
;      CITY:  Salt Lake City
;      STATE:  Utah
;      COUNTRY:  USA
;      ZIP:  84110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
```

```
;      APPLICATION NUMBER:  US/08/470,179
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sweigert Ph.D, Susan E.
;      REGISTRATION NUMBER:  36,289
;      REFERENCE/DOCKET NUMBER:  2601
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  801-532-1922
;      TELEFAX:  801-531-9168
;  INFORMATION FOR SEQ ID NO:  111:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  423 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Arthrobacter globiformis
US-08-470-179-111

  Query Match             49.7%;  Score 19.4;  DB 1;  Length 423;
  Best Local Similarity   79.3%;  Pred. No. 64;
  Matches   23;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      4 agatggccttggtggccttggaaatggcc 32
          |||||||   | ||||| ||||||||| |
Db    263 AGATGGCACCGCTGGCCATGGAAATGGTC 291

RESULT  11
US-08-470-179-147
; Sequence 147, Application US/08470179
; Patent No. 5645994
;  GENERAL INFORMATION:
;    APPLICANT:  Huang Ph.D, Wai Mun
;    TITLE OF INVENTION:  Method and Compositions for
;    TITLE OF INVENTION:  Identification of Species in a Sample
;    NUMBER OF SEQUENCES:  207
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Trask, Britt and Rossa
;      STREET:  P.O. Box 2550
;      CITY:  Salt Lake City
;      STATE:  Utah
;      COUNTRY:  USA
;      ZIP:  84110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,179
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sweigert Ph.D, Susan E.
;      REGISTRATION NUMBER:  36,289
;      REFERENCE/DOCKET NUMBER:  2601
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  801-532-1922
;      TELEFAX:  801-531-9168
;  INFORMATION FOR SEQ ID NO:  147:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  423 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Micrococcus leteus
US-08-470-179-147

  Query Match             49.7%;  Score 19.4;  DB 1;  Length 423;
  Best Local Similarity   79.3%;  Pred. No. 64;
  Matches   23;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      4 agatggccttggtggccttggaaatggcc 32
          ||||||||   | ||||| |||| |||| |
Db    263 AGATGGCCCCGCTGGCCATGGAGATGGTC 291

RESULT  12
US-09-248-588-12
; Sequence 12, Application US/09248588
; Patent No. 6231864
; GENERAL INFORMATION:
;  APPLICANT: Birkett, Ashley J.
;  TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and
;  TITLE OF INVENTION: their Derivatives
;  FILE REFERENCE: SYN-101 4564/69529
;  CURRENT APPLICATION NUMBER: US/09/248,588
;  CURRENT FILING DATE: 1999-02-11
;  EARLIER APPLICATION NUMBER: 60/074537
;  EARLIER FILING DATE: 1998-02-12
;  NUMBER OF SEQ ID NOS: 113
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 918
;   TYPE: DNA
;   ORGANISM: Hepatitis B virus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(915)
US-09-248-588-12

  Query Match             49.7%;  Score 19.4;  DB 4;  Length 918;
  Best Local Similarity   79.3%;  Pred. No. 73;
  Matches   23;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      1 aggagatggccttggtggccttggaaatg 29
          ||||||| || |||||||| ||  || ||
Db    559 aggagattgctttggtggcattacaactg 587

RESULT  13
PCT-US96-10602-9
; Sequence 9, Application PC/TUS9610602
;  GENERAL INFORMATION:
;    APPLICANT:  The General Hospital Corporation
;    TITLE OF INVENTION:  INHIBITION OF HEPATITIS B REPLICATION
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/10602
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
```

```
;       APPLICATION NUMBER:  60/017,814
;       FILING DATE:  20-JUN-1995
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Clark, Paul T.
;       REGISTRATION NUMBER:  30,162
;       REFERENCE/DOCKET NUMBER:  00786/282001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617/542-5070
;       TELEFAX:  617/542-8906
;       TELEX:  200154
;   INFORMATION FOR SEQ ID NO:  9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1263 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA
PCT-US96-10602-9


  Query Match             49.7%;  Score 19.4;  DB 5;  Length 1263;
  Best Local Similarity   79.3%;  Pred. No. 78;
  Matches   23;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      1 aggagatggccttggtggccttggaaatg 29
          ||||||| || ||||||||| ||  || ||
Db    430 AGGAGATTGCTTTGGTGGCATTACAACTG 458

RESULT  14
US-08-391-000-41
; Sequence 41, Application US/08391000
; Patent No. 5723752
;  GENERAL INFORMATION:
;    APPLICANT:  HOUTZ, Robert L.
;    TITLE OF INVENTION:  CLONING AND DEVELOPMENTAL EXPRESSION OF
;    TITLE OF INVENTION:  PEA RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
;    TITLE OF INVENTION:  SUBUNIT N-METHYLTRANSFERASE
;    NUMBER OF SEQUENCES:  41
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  P.O. Box 1404
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/391,000
;      FILING DATE:  21-FEB-1995
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meuth, Donna M.
;      REGISTRATION NUMBER:  36,607
;      REFERENCE/DOCKET NUMBER:  028750-123
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  41:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1801 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  59..1528
US-08-391-000-41


  Query Match             49.7%;  Score 19.4;  DB 1;  Length 1801;
  Best Local Similarity   70.3%;  Pred. No. 83;
  Matches   26;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy      2 ggagatggccttggtggccttggaaatggcctcttat 38
          || |||  |||||| | ||| |||||   | ||| ||
Db   1493 GGCGATATCCTTGGAGACCTAGGAAAATTCTTCTAAT 1529

RESULT  15
US-08-741-931-41
; Sequence 41, Application US/08741931
; Patent No. 5866394
;  GENERAL INFORMATION:
;    APPLICANT:  HOUTZ, Robert L.
;    TITLE OF INVENTION:  CLONING AND DEVELOPMENTAL EXPRESSION OF
;    TITLE OF INVENTION:  PEA RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
;    TITLE OF INVENTION:  SUBUNIT N-METHYLTRANSFERASE
;    NUMBER OF SEQUENCES:  41
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  P.O. Box 1404
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/741,931
;      FILING DATE:  31-OCT-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/391,000
;      FILING DATE:  21-FEB-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meuth, Donna M.
;      REGISTRATION NUMBER:  36,607
;      REFERENCE/DOCKET NUMBER:  028750-123
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  41:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1801 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  59..1528
US-08-741-931-41


  Query Match             49.7%;  Score 19.4;  DB 2;  Length 1801;
  Best Local Similarity   70.3%;  Pred. No. 83;
  Matches   26;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy      2 ggagatggccttggtggccttggaaatggcctcttat 38
          || |||  |||||| | ||| |||||   | ||| ||
Db   1493 GGCGATATCCTTGGAGACCTAGGAAAATTCTTCTAAT 1529


Search completed: January 29, 2002, 21:24:42
Job time: 1720 sec
```